

Human protein: Q8TBE1 - Cornichon-like protein. - EMBL Bioinformatic HarvesterEMBL-Heidelberg - [harvester \(c\)](#) - [technology](#) - [gfp-cdna](#) - [pepperkok-team](#) - [contact](#) -Length: **160 aa**, molecular weight: **18976 Da**, CRC64 checksum: **CF7E8645A9587504**

MAFTFAAF	FCY	MLSLVL	CAAL	IFFAIW	HIIA	FDELRT	DFKS	PIDQCN	PVHA	RERLRN	IERI	60		
CFLLRK	LVL	P	EYSIHS	LF	CI	MFLCAQ	EWLT	LGLNV	PLLFY	HFWR	YFHCPA	DSSE	LAYDPP	120
VVMNAD	TL	SY	CQKEAW	CKLA	FYLLS	FFYYL	YCMIY	TLVSS						160

//

GoTo: EBI - Hinxton - "SWALL" database**General information**Entry name **CNIL_HUMAN**Accession number **Q8TBE1**

Created Rel. 41, 28-FEB-2003

Sequence update Rel. 41, 28-FEB-2003

Annotation update Rel. 42, 15-SEP-2003

Description and origin of the Protein

Description Cornichon-like protein.

Gene name(s) CNIL.

Organism source Homo sapiens (Human).

Taxonomy Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI TaxID 22388257

PubMed AK096312;[BAC04760.1](#);.[BC022780](#);[AAH22780.1](#);.

InterPro PF03311;Cornichon;1.

PROSITE Transmembrane;

Features

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Key	Begin	End	Length	Description
<u>TRANSMEM</u>	11	31	21	POTENTIAL.
<u>TRANSMEM</u>	73	93	21	POTENTIAL.
<u>TRANSMEM</u>	139	159	21	POTENTIAL.

Activate BLAST of: Q8TBE1

	BLAST	Pro
	Genome	Nucle

Query: gi|21755779 hypothetical protein FLJ38993 [Homo sapiens]

Matching gi: 18490801, 26329545, 27805431, 22749039

Best hits

Common Tree

Taxonomy Report

3D structures

CDD-Search

Gelis

31 BLAST hits to 12 unique species Sort by taxonomy proximity

Archaea

Bacteria

Metazoa

Fungi

Plants

Viruses

Other Eukaryotae

Keep only


























Cut-Off 100

Select

Reset

160 aa

	SCORE	P	ACCESSION	GI	PROTEIN DESCRIPTION
	847	21	BAB28996	12851288	unnamed protein product [Mu
	729	21	BAA21746	4521254	cornichon-like protein [Mus
	578	21	AAC15828	2460430	cornichon [Mus musculus]
	577	27	AAC98388	4063709	cornichon [Homo sapiens]
	521	27	AAD32301	4894209	cornichon-like protein [Hom
	499	10	AAK15762	13195570	cornichon [Boltenia villosa
	403	8	AAA86527	886769	cni gene product
	401	8	P52159	1705957	CORNICHON PROTEIN
	390	8	EAA14788	30174276	ENSANGP00000019460 [Anophel
	389	7	CAB01516	5824608	Hypothetical protein T09E8.
	359	27	CAD62612	28207917	unnamed protein product [Ho
	355	7	A89261	25336821	protein T09E8.3 [imported]
	207	21	BAB32366	12862150	unnamed protein product [Mu
	205	27	AAF29127	6841548	HSPC163 [Homo sapiens]
	203	21	XP_213960	27679416	similar to RIKEN cDNA D5300
	176	21	XP_136930	20853677	similar to cornichon homolo
	174	4	EAA30033	28920672	hypothetical protein [Neuro
	159	4	CAA96756	1322550	ORF YGL054c [Saccharomyces
	156	4	CAB90792	7768496	putative er-derived vesicle
	154	8	EAA14707	21302562	ENSANGP00000010644 [Anophel
	154	8	AAF51153	7295853	CG17262-PA [Drosophila mela
	152	7	AAK39349	13775541	Hypothetical protein Y64H9A
	128	4	CAB16265	2414616	putative er-derived vesicle

S.O.U.R.C.E.
SearchGeneReport for:
AK096312

Help



SOURCE
GeneReport
181 sequences

FLJ38993

hypothetical protein FLJ38993

[UniGene](#), [LocusLink](#), [OMIM](#), [GenAtlas](#), [GeneCard](#), [Ensembl](#), [MapView](#), [Genome Browser](#)

Chromosomal Location

Chromosome/Cytoband 1q42.12

Annotations

Gene Ontologies	Ontology	Annotation	Evidence	Sour
	Biological Process	Intracellular signaling cascade	IEA	GOA
	Cellular Component	Integral to membrane	IEA	GOA

UniGene & EST Expression Information

UniGene Cluster	Hs.13410 from Build No. 160 , Released on 2003-03-29		
Normalized expression distribution for tissue type Top ten [of 13] [Help]	Tissue	Normalized Expression (%)	Cluster Clones : Tissue clon
	malignant melanoma, metastatic to lymph node:	22.22	1:2723
	testis:	11.62	1:5207
	total brain:	11.57	2:10454
	large cell carcinoma, undifferentiated:	10.73	1:5637
	melanotic melanoma:	10.36	10:58397
	glioblastoma with EGFR amplification:	7.25	1:8343
	medulla:	6.60	1:9172
	hippocampus:	6.52	2:18566
	melanotic melanoma, high MDR (cell line):	5.91	1:10228
	melanotic melanoma, cell line:	3.34	1:18104
SAGE (NCBI)	Go to Gene-to-tag Mapping at NCBI		

Upstream Genomic Sequence

TRASER	Upstream genomic sequence for hypothetical protein FLJ38993
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Representative mRNA Sequences

UniGene	NM_152495	
LocusLink RefSeq	Accession	Description
	NM_152495	NA

Alias PubMed Search

[PubMed](#)[Search PubMed using aliases AND](#)[PubMed](#)[Search](#)[No Clone Report](#)[Help](#)[ACTIVATE: SMART analysis](#)

name	begin	end	E-value
Pfam:Cornichon	6	152	1.20e-68

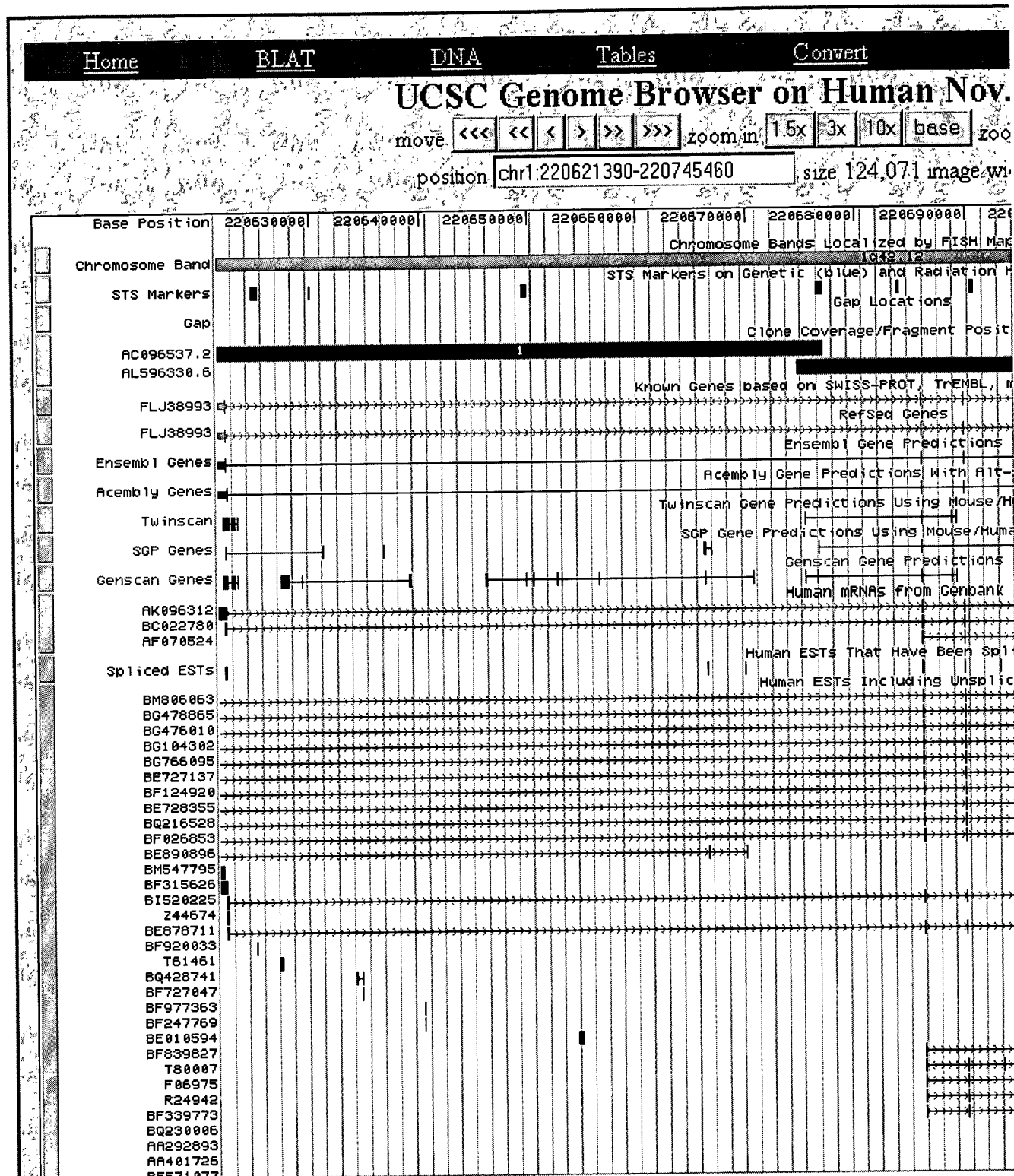
These features and domains are not shown in the diagram, either because their scores are less significant than the required threshold, or because they overlap with some other source of annotation:

name	begin	end	E-value	reason
signal peptide	1	18	-	overlap
transmembrane	7	29	-	overlap
transmembrane	77	99	-	overlap
transmembrane	139	158	-	overlap
low complexity	139	151	-	overlap

Summary of BLAST results. Note that the probabilities are not directly comparable to those in the table above.

name	seq	begin	end	E-value
SCOP:d1erza	d1erza		44	5.30e+00
SCOP:d1eija	d1eija	50	71	3.10e+00

[Activate IPsort of:Q8TBE1](#)[Activate Genome Browser of: Q8TBE1](#)



[Activate MapView of: Q8TBE1](#)

NCBI
PubMed Entrez BLAST OMIM

Search Find in This View

Homo sapiens Map View build 33 **BLAST the Human Genome**

Chromosome: [1] 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y

Query: AK096312>all matches [clear]

Master Map: Genes On Sequence **Maps & Options**

Total Genes On Chromosome: 3232 [153 not localized]
Region Displayed: 215M-222M bp [Download/View Sequence/Evidence](#)
Genes Labeled: 20 Total Genes in Region: 84

Gene...	HsUniG	Genes_seq	symbol	links
		216M	DKFZp547M236	+ sv ev - seq mr
			RAB3-GAP150	+ sv ev - seq mr
		217M	FLJ14146	+ sv ev - seq mr
			FLJ20605	+ sv ev - seq mr
			DUSP10	+ sv ev hm seq m
		218M	FLJ13840	+ sv ev hm seq m
			DISPA	+ sv ev hm seq m
			FLJ35728	+ sv ev - seq mr
		219M	CAPN2	+ sv ev hm seq m
			TP53BP2	+ sv ev - seq mr
			FLJ38993	+ sv ev - seq mr
		220M	LBR	+ sv ev - seq mr
			PRO0650	+ sv ev - seq mr
			EPHX1	+ sv ev hm seq m
		221M	KIAA0792	+ sv ev - seq mr
			LEFTB	+ sv ev hm seq m
			EBAF	+ sv ev hm seq m
		222M	FLJ35382	+ sv ev - seq mr
			GOCAP1	+ sv ev - seq mr
			MIXL1	+ sv ev - seq mr

Region Shown: 215981389 222838203

out 200M in

ideogram master

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Activate: STRING of: Q8TBE1

[Home](#)[Download](#)[Help/Info](#)**STRING****No predictions found ...**

Sorry, we have not found any functional associations in our database.

Your input was 'Q8TBE1' (Similar to RIKEN cDNA 2900075G08 gene).

This gene is not a member of an orthologous group, which is a prerequisite for genomic context methods.

Please note that STRING works best for prokaryotes, although it contains many predictions for eukaryotes as well - mainly in the areas metabolism and information processing.

Orthology information is derived from the COG database, which we extended to cover more species and more genes, using an automatic update mechanism.

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[Activate: Conserved Domains of: Q8TBE1](#)



ACTIVATE: SOSUI analysis

This amino acid sequence is of a MEMBRANE PROTEIN
which have 3 transmembrane helices.

No.	N terminal	transmembrane region	C terminal	type	length
1	7	AFCYMLSLVLCAALIFFAIWHII	29	PRIMARY	23
2	81	MFLCAQEWLTLGLNVPLLFYHFW	103	SECONDARY	23
3	136	WCKLAFYLLSFFYYLYCMIYTLV	158	PRIMARY	23

ACTIVATE: IPSORT analysis**iPSORT Prediction**

Predicted as: *having a signal peptide*

Sequence (Type: nonplant)

1 MAFTF AAFCY MSLSV LCAAL IFFAI WHIIA FDEL R TDFKS PIDQC NPVHA
51 RERLR NIERI CFLLR KLVLP EYSIH SLFCI MFLCA QEWT LGLNV PLLFY
101 HFWRY FHCPA DSSEL AYDPP VMNA DTLSY CQKEA WCKLA FYLLS FFYYL
151 YCMIY TLVSS

Values used for reasoning

Node	Answer	View	Substring	Value(s)	Plot
1. Signal peptide?	Yes	Average Hydropathy (KYTJ820101)	[6,20]	2.28 (≥ 0.953 ? Yes)	show
2. Mitochondrial ?	No	Average Net Charge (KLEP840101)	[1,30]	0 (≥ 0.083 ? No)	show
		Indexing: AI1 Pattern: 221121122 (ins/del ≤ 3)	[1,30]	MAFTFAAFCYMLSLVLCAA--L-IFFAIWHIIA 22222222222222222222--2-1222120112 221121122	--

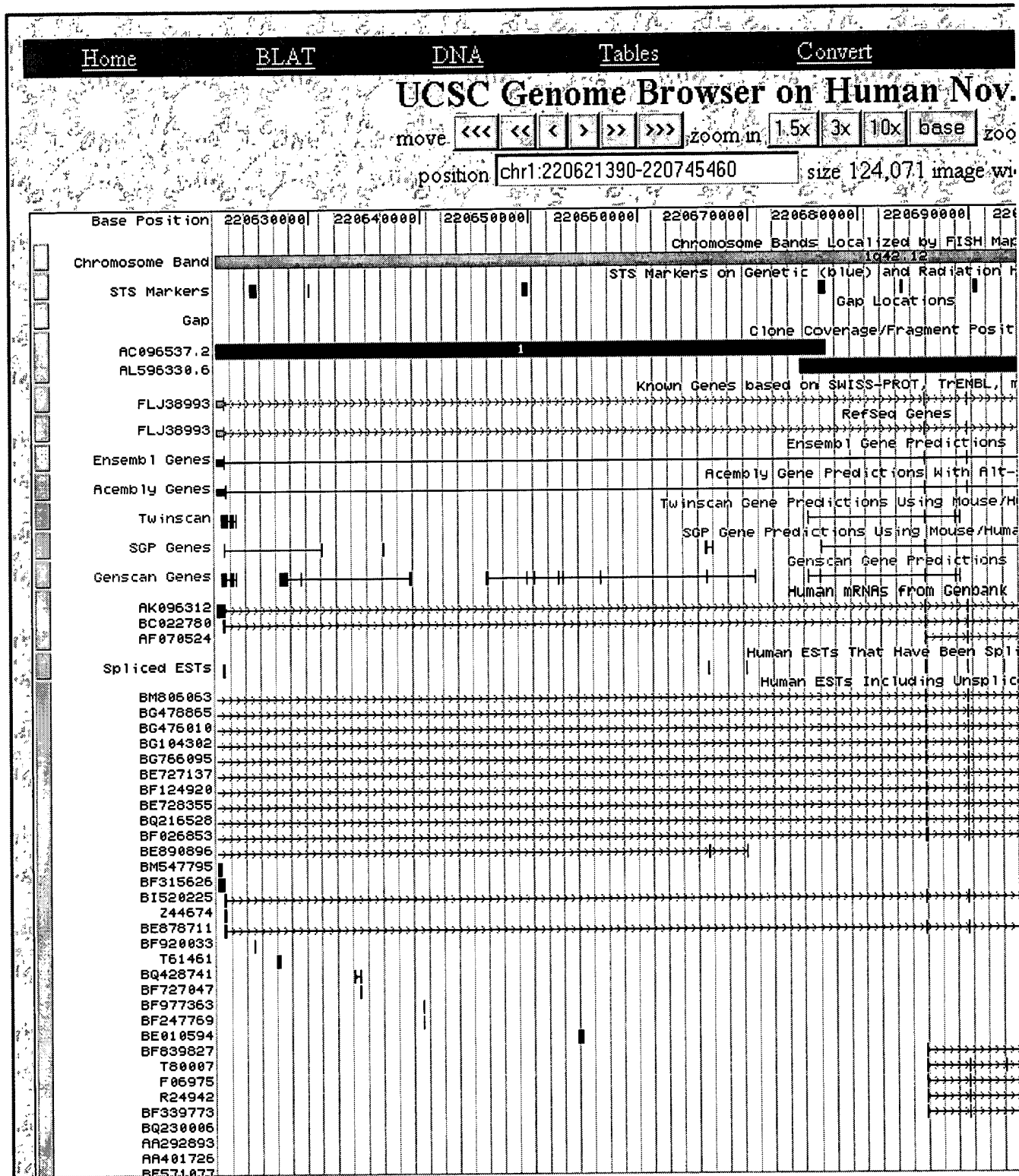
* This color means "not used".

Name	Alphabet Indexing		
	0	1	2

AI1	DEGHKN	IR	ACFLMPQSTVWY
AI2	ACDEFGHLMNQSTVWY	KR	IP

[Return to iPSORT Home](#)

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NCBI
PubMed Entrez BLAST OMIM

Search Find in This View

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Total Genes On Chromosome: 3232 [153 not localized]
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Region Shown: 215981389 222838203 Go

out 200M in

ideogram master

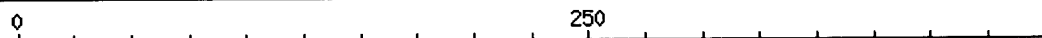
Gene...	HsUniG	Genes_seq	symbol	links
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			PRO0650	sv ev - seq mrr
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			LEFTB	sv ev hm seq m
			EBAF	sv ev hm seq m
		222M	FLJ35382	sv ev - seq mrr
			GOCAP1	sv ev - seq mrr
			MIXL1	sv ev - seq mrr

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Activate CDART of:Q8TBE1



CDART: Conserved Domain Architecture Retrieval Tool

[New Query](#)[Overview](#)[PubMed](#)[Nucleotide](#)[Protein](#)[Structure](#)[Taxonomy](#)



Query 

[more>](#)Similar domain architectures

35 Sequences 
Eukaryota
Cornichon-like pro

AAF79631 
Arabidopsis thaliana
F5011.7

[more>](#)Result page: [Previous](#) 1 [Next](#) by Taxonomy by selected domains:

- ☐  [pfam03311](#) Cornichon protein.
- ☐  [pfam04127](#) DNA / pantothenate metabolism flavoprotein. The D...
includes: [COG0163](#) [COG0452](#) [COG1036](#) [pfam02441](#)

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[NCBI](#) | [NLM](#) | [NIH](#)

Activate SOSUI of:Q8TBE1

SOSUI Result

Query title :

Total length : 160 A. A.

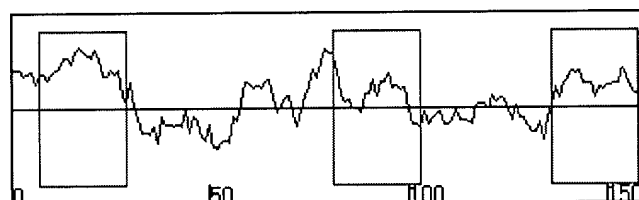
Average of hydrophobicity : 0.600000

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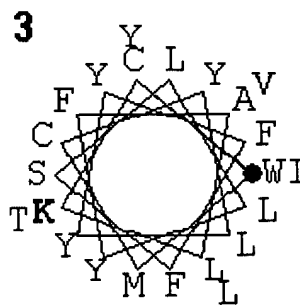
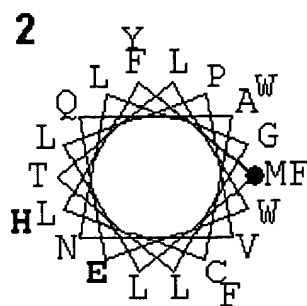
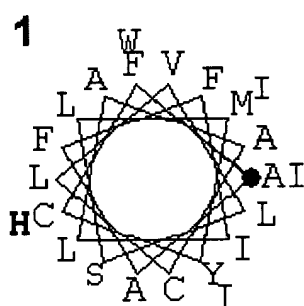
Display Options

[Hydropathy profile]



[Helical wheel diagram of predicted segments]

Hydrophobic residue: Black
Polar residue: Blue
Charged residue: Bold blue(+) Bold red(-)



Activate: STRING of: Q8TBE1

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